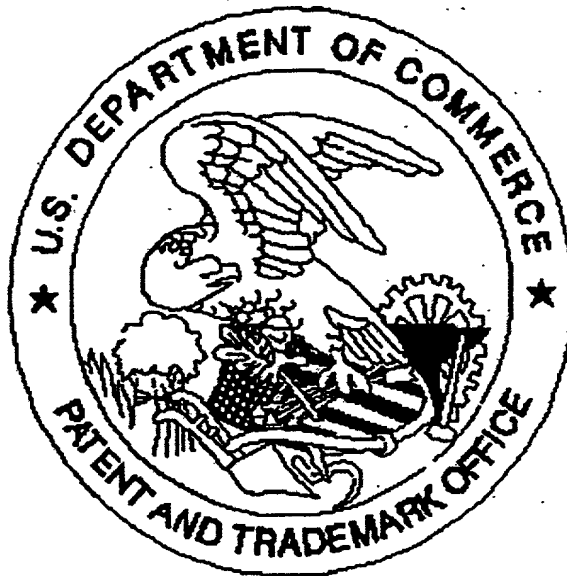


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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the application of: Bates, *et al.*

Serial No.: Not Yet Assigned

Filed: Herewith (December 21, 2001)

**For: NOVEL GLUTAMATE RECEPTOR
MODULATORY PROTEINS AND NUCLEIC
ACID MOLECULES AND USES THEREFOR**

Attorney Docket No.: GNN-024

Commissioner for Patents

Box Sequence

Washington, D.C. 20231

TRANSMITTAL LETTER FOR DISKETTE CONTAINING SEQUENCE LISTING

Dear Sir:

Enclosed is a diskette which contains a computer readable form of the Sequence Listing for the patent application filed herewith. The Sequence Listing complies with the requirements of 37 C.F.R. §1.821. The material on this diskette is identical in substance to the sequence listing appearing on pages 1-16 of the Sequence Listing which is submitted herewith, as required by 37 C.F.R. §1.821(f). The computer readable form of the sequence listing contained on the enclosed diskette is understood to comply with the requirements of §1.824(d).

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Signature

Larry Taylor

Please Print Name of Person Signing

Respectfully submitted,

LAHIVE & COCKFIELD, LLP

By: 

Elizabeth A. Hanley, Esq.

Registration No. 33,505 *for*

Debra J. Milasincic, Esq.

Registration No. 46,931

Attorney for Applicants

Date: December 21, 2001

SEQUENCE LISTING

<110> Brian Gaither Bates
Kamalaka Gulukota
Yuhong Xie
Janet Elizabeth Paulsen

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NUCLEIC ACID MOLECULES AND USES THEREFOR

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Gln	Thr	Ala	Val	Ile	Lys	Pro	Phe	Pro	Lys	Ser	Thr	Glu	Ser	Arg	Gly				
945					950					955					960				
Leu	Gly	Ala	Gly	Ala	Gly	Ala	Gly	Gly	Ser	Ala	Gly	Gly	Val	Gly	Ala				
965					970					975									
Thr	Gly	Gly	Ala	Gly	Cys	Ala	Gly	Ala	Gly	Pro	Gly	Gly	Pro	Glu	Ser				
980					985					990									
Pro	Asp	Ala	Gly	Pro	Lys	Ala	Leu	Tyr	Asp	Val	Ala	Glu	Ala	Glu	Glu				
995					1000					1005									
His	Phe	Pro	Ala	Pro	Ala	Arg	Pro	Arg	Ser	Pro	Ser	Pro	Ile	Ser	Thr				
1010					1015					1020									
Leu	Ser	His	Arg	Ala	Gly	Ser	Ala	Ser	Arg	Thr	Asp	Asp	Asp	Val	Pro				
1025					1030					1035					1040				
Ser	Leu	His	Ser	Glu	Pro	Val	Ala	Arg	Ser	Ser	Ser	Ser	Gln	Gly	Ser				
1045					1050					1055									
Leu	Met	Glu	Gln	Ile	Ser	Ser	Val	Val	Thr	Arg	Phe	Thr	Ala	Asn	Ile				
1060					1065					1070									
Ser	Glu	Leu	Asn	Ser	Met	Met	Leu	Ser	Thr	Ala	Ala	Pro	Ser	Pro	Gly				
1075					1080					1085									
Val	Gly	Ala	Pro	Leu	Cys	Ser	Ser	Tyr	Leu	Ile	Pro	Lys	Glu	Ile	Gln				
1090					1095					1100									
Leu	Pro	Thr	Thr	Met	Thr	Thr	Phe	Ala	Glu	Ile	Gln	Pro	Leu	Pro	Ala				
1105					1110					1115					1120				
Ile	Glu	Val	Thr	Gly	Gly	Ala	Gln	Pro	Ala	Ala	Gly	Ala	Gln	Ala	Ala				
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Ala	Lys	Pro	Asp	Leu	Glu	Glu	Leu	Val	Ala	Leu	Thr	Pro	Pro	Ser	Pro				
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Phe	Arg	Asp	Ser	Val	Asp	Ser	Gly	Ser	Thr	Thr	Pro	Asn	Ser	Pro	Val				
1170					1175					1180									
Ser	Glu	Ser	Ala	Leu	Cys	Ile	Pro	Ser	Ser	Pro	Lys	Tyr	Asp	Thr	Leu				
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Ile	Ile	Arg	Asp	Tyr	Thr	Gln	Ser	Ser	Ser	Ser	Leu								

1210

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Asp Lys Leu Leu Lys Lys Leu Arg Ser His Leu Pro Lys Ala Arg Val
 260 265 270
 Val Ala Cys Phe Cys Glu Gly Met Thr Val Arg Gly Leu Leu Met Ala
 275 280 285
 Met Arg Arg Leu Gly Leu Ala Gly Glu Phe Leu Leu Gly Ser Asp
 290 295 300
 Gly Trp Ala Asp Arg Tyr Asp Val Thr Asp Gly Tyr Gln Arg Glu Ala
 305 310 315 320
 Val Gly Gly Ile Thr Ile Lys Leu Gln Ser Pro Asp Val Lys Trp Phe
 325 330 335
 Asp Asp Tyr Tyr Leu Lys Leu Arg Pro Glu Thr Asn Leu Arg Asn Pro
 340 345 350
 Trp Phe Gln Glu Phe Trp Gln His Arg Phe Gln Cys Arg Leu Glu Gly
 355 360 365
 Phe Ala Gln Glu Asn Ser Lys Tyr Asn Lys Thr Cys Asn Ser Ser Leu
 370 375 380
 Thr Leu Arg Thr His His Val Gln Asp Ser Lys Met Gly Phe Val Ile
 385 390 395 400
 Asn Ala Ile Tyr Ser Met Ala Tyr Gly Leu His Asn Met Gln Met Ser
 405 410 415
 Leu Cys Pro Gly Tyr Ala Gly Leu Cys Asp Ala Met Lys Pro Ile Asp
 420 425 430
 Gly Arg Lys Leu Leu Asp Ser Leu Met Lys Thr Asn Phe Thr Gly Val
 435 440 445
 Ser Gly Asp Met Ile Leu Phe Asp Glu Asn Gly Asp Ser Pro Gly Arg
 450 455 460
 Tyr Glu Ile Met Asn Phe Lys Glu Met Gly Lys Asp Tyr Phe Asp Tyr
 465 470 475 480
 Ile Asn Val Gly Ser Trp Asp Asn Gly Glu Leu Lys Met Asp Asp Asp
 485 490 495
 Glu Val Trp Ser Lys Lys Asn Asn Ile Ile Arg Ser Val Cys Ser Glu
 500 505 510
 Pro Cys Glu Lys Gly Gln Ile Lys Val Ile Arg Lys Gly Glu Val Ser
 515 520 525
 Cys Cys Trp Thr Cys Thr Pro Cys Lys Glu Asn Glu Tyr Val Phe Asp
 530 535 540
 Glu Tyr Thr Cys Lys Ala Cys Gln Leu Gly Ser Trp Pro Thr Asp Asp
 545 550 555 560

Leu Thr Gly Cys Asp Leu Ile Pro Val Gln Tyr Leu Arg Trp Gly Asp
 565 570 575
 Pro Glu Pro Ile Ala Ala Val Val Phe Ala Cys Leu Gly Leu Leu Ala
 580 585 590
 Thr Leu Phe Val Thr Val Ile Phe Ile Ile Tyr Arg Asp Thr Pro Val
 595 600 605
 Val Lys Ser Ser Ser Arg Glu Leu Cys Tyr Ile Ile Leu Ala Gly Ile
 610 615 620
 Cys Leu Gly Tyr Leu Cys Thr Phe Cys Leu Ile Ala Lys Pro Lys Gln
 625 630 635 640
 Ile Tyr Cys Tyr Leu Gln Arg Ile Gly Ile Gly Leu Ser Pro Ala Met
 645 650 655
 Ser Tyr Ser Ala Leu Val Thr Lys Thr Asn Arg Ile Ala Arg Ile Leu
 660 665 670
 Ala Gly Ser Lys Lys Lys Ile Cys Thr Lys Lys Pro Arg Phe Met Ser
 675 680 685
 Ala Cys Ala Gln Leu Val Ile Ala Phe Ile Leu Ile Cys Ile Gln Leu
 690 695 700
 Gly Ile Ile Val Ala Leu Phe Ile Met Glu Pro Pro Asp Ile Met His
 705 710 715 720
 Asp Tyr Pro Ser Ile Arg Glu Val Tyr Leu Ile Cys Asn Thr Thr Asn
 725 730 735
 Leu Gly Val Val Thr Pro Leu Gly Tyr Asn Gly Leu Leu Ile Leu Ser
 740 745 750
 Cys Thr Phe Tyr Ala Phe Lys Thr Arg Asn Val Pro Ala Asn Phe Asn
 755 760 765
 Glu Ala Lys Tyr Ile Ala Phe Thr Met Tyr Thr Thr Cys Ile Ile Trp
 770 775 780
 Leu Ala Phe Val Pro Ile Tyr Phe Gly Ser Asn Tyr Lys Ile Ile Thr
 785 790 795 800
 Met Cys Phe Ser Val Ser Leu Ser Ala Thr Val Ala Leu Gly Cys Met
 805 810 815
 Phe Val Pro Lys Val Tyr Ile Ile Leu Ala Lys Pro Glu Arg Asn Val
 820 825 830
 Arg Ser Ala Phe Thr Thr Ser Thr Val Val Arg Met His Val Gly Asp
 835 840 845
 Gly Lys Ser Ser Ser Ala Ala Ser Arg Ser Ser Ser Leu Val Asn Leu
 850 855 860

Trp Lys Arg Arg Gly Ser Ser Gly Glu Thr Leu Arg Tyr Lys Asp Arg
 865 870 875 880
 Arg Leu Ala Gln His Lys Ser Glu Ile Glu Cys Phe Thr Pro Lys Gly
 885 890 895
 Ser Met Gly Asn Gly Gly Arg Ala Thr Met Ser Ser Ser Asn Gly Lys
 900 905 910
 Ser Val Thr Trp Ala Gln Asn Glu Lys Ser Thr Arg Gly Gln His Leu
 915 920 925
 Trp Gln Arg Leu Ser Val His Ile Asn Lys Lys Glu Asn Pro Asn Gln
 930 935 940
 Thr Ala Val Ile Lys Pro Phe Pro Lys Ser Thr Glu Asn Arg Gly Pro
 945 950 955 960
 Gly Ala Ala Ala Gly Gly Gly Ser Gly Pro Gly Val Ala Gly Ala Gly
 965 970 975
 Asn Ala Gly Cys Thr Ala Thr Gly Gly Pro Glu Pro Pro Asp Ala Gly
 980 985 990
 Pro Lys Ala Leu Tyr Asp Val Ala Glu Ala Glu Glu Ser Phe Pro Ala
 995 1000 1005
 Ala Ala Arg Pro Arg Ser Pro Ser Pro Ile Ser Thr Leu Ser His Leu
 1010 1015 1020
 Ala Gly Ser Ala Gly Arg Thr Asp Asp Asp Ala Pro Ser Leu His Ser
 1025 1030 1035 1040
 Glu Thr Ala Ala Arg Ser Ser Ser Ser Gln Gly Ser Leu Met Glu Gln
 1045 1050 1055
 Ile Ser Ser Val Val Thr Arg Phe Thr Ala Asn Ile Ser Glu Leu Asn
 1060 1065 1070
 Ser Met Met Leu Ser Thr Ala Ala Thr Pro Gly Pro Pro Gly Thr Pro
 1075 1080 1085
 Ile Cys Ser Ser Tyr Leu Ile Pro Lys Glu Ile Gln Leu Pro Thr Thr
 1090 1095 1100
 Met Thr Thr Phe Ala Glu Ile Gln Pro Leu Pro Ala Ile Glu Val Thr
 1105 1110 1115 1120
 Gly Gly Ala Gln Gly Ala Thr Gly Val Ser Pro Ala Gln Glu Thr Pro
 1125 1130 1135
 Thr Gly Ala Glu Ser Ala Pro Gly Lys Pro Asp Leu Glu Glu Leu Val
 1140 1145 1150
 Ala Leu Thr Pro Pro Ser Pro Phe Arg Asp Ser Val Asp Ser Gly Ser
 1155 1160 1165

Thr Thr Pro Asn Ser Pro Val Ser Glu Ser Ala Leu Cys Ile Pro Ser
 1170 1175 1180

Ser Pro Lys Tyr Asp Thr Leu Ile Ile Arg Asp Tyr Thr Gln Ser Ser
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Ser Ser Leu

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 <223> Leu, Ile, Val or Met

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 <223> Description of Artificial Sequence:consensus
 sequence

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